10/3,AB/3 (Item 3 f[redacted] file: 155)
DIALOG(R)File 155:MEDLINE(R)

09266302 97188567 PMID: 9037152
Engineering resistance against **tomato yellow leaf curl virus** (TYLCV) using antisense RNA.
Bendahmane M; Gronenborn B
Centre National de la Recherche Scientifique, Gif-sur-Yvette, France.
Plant molecular biology (NETHERLANDS) Jan 1997, 33 (2) p351-7, ISSN 0167-4412 Journal Code: A6O
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
One of the most severe diseases of cultivated **tomato** worldwide is caused by **tomato yellow leaf curl virus** (TYLCV), a geminivirus transmitted by the whitefly Bemisia tabaci. Here we describe the application of antisense RNAs to interfere with the disease caused by TYLCV. The target of the antisense RNA is the rare messenger RNA of the **Rep protein**, encoded by the C1 gene. Transgenic Nicotiana benthamiana plants expressing C1 antisense RNA were obtained and shown to resist infection by TYLCV. Some of the resistant lines are symptomless, and the replication of challenge TYLCV almost completely suppressed. The transgenes mediating resistance were shown to be effective through at least two generations of progeny.

10/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09018873 97015759 PMID: 8862407
Resistance to **tomato yellow leaf curl** geminivirus in Nicotiana benthamiana plants transformed with a truncated viral C1 gene.
Noris E; Accotto GP; Tavazza R; Brunetti A; Crespi S; Tavazza M
Istituto di Fitovirologia Applicata, National Research Council, Turin, Italy.
Virology (UNITED STATES) Oct 1 1996, 224 (1) p130-8, ISSN 0042-6822 Journal Code: XEA
Erratum in Virology 1997 Jan 20;227(2) 519
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
The C1 gene of **tomato yellow leaf curl** geminivirus (TYLCV) encodes a multifunctional **protein** (**Rep**) involved in replication. A truncated form of this gene, capable of expressing the N-terminal 210 amino acids (aa) of the **Rep protein**, was cloned under the control of the CaMV 35S promoter and introduced into Nicotiana benthamiana using Agrobacterium tumefaciens. The same sequence was also cloned in antisense orientation. When self-pollinated progeny of 19 primary transformants were tested for resistance to TYLCV by agroinoculation, some plants proved to be resistant, particularly in the sense lines. Two such lines were further studied. The presence of the transgene was verified and its expression was followed at intervals. All plants that were resistant to TYLCV at 4 weeks postinoculation (wpi) contained detectable amounts of transgenic mRNA and **protein** at the time of infection. Resistance was overcome in a few plants at 9 wpi, and in most at 15 wpi. Infection of **leaf** discs derived from transgenic plants showed that expression of the transgene correlated with a substantial reduction of viral DNA replication. Cotransfections of tobacco protoplasts demonstrated that inhibition of viral DNA replication requires expression of the truncated **Rep protein** and suggested that the small ORF C4, also present in our construct, plays no role in the resistance observed. The results obtained using both transient and stable gene expression systems show that the expression of the N-terminal 210 aa of the TYLCV **Rep protein** efficiently interferes with **virus** infection.

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          188570  YELLOW
          682252  LEAF?
            9521  CURL
         2169977  VIRUS?
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            1667  S6
             191  REP?2
      S7       0  S6 AND REP?2
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         6203817  PROTEIN?
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            1667  S6
      S9      71  S8 AND S6
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>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
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>>>Record 266:276441 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:275036 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:272648 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:263053 ignored; incomplete bibliographic data, not retained -
in RD set
...completed examining records
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 10/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11533964   21326165   PMID: 11342533
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Expression of the oligomerization domain of the replication-associated **protein** (**Rep**) of **Tomato leaf curl** New Delhi **virus** interferes with DNA accumulation of heterologous geminiviruses.

Chatterji A; Beachy RN; Fauquet CM

International Laboratory for Tropical Agricultural Biotechnology, Donald Danforth Plant Science Center, 8001 Natural Bridge Road, St. Louis, MO 63121, USA.

Journal of biological chemistry (United States) Jul 6 2001, 276 (27) p25631-8, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The minimal DNA binding domain of the replication-associated **protein** (**Rep**) of **Tomato leaf curl** New Delhi **virus** was determined by electrophoretic mobility gel shift analysis and co-purification assays. DNA binding activity maps to amino acids 1-160 (**Rep**-(1-160)) of the **Rep protein** and overlaps with the **protein** oligomerization domain. Transient expression of **Rep protein** (**Rep**-(1-160)) was found to inhibit homologous viral DNA accumulation by 70-86% in tobacco protoplasts and in Nicotiana benthamiana plants. The results obtained showed that expression of N-terminal sequences of **Rep protein** could efficiently interfere with DNA binding and oligomerization activities during **virus** infection. Surprisingly, this **protein** reduced accumulation of the African cassava mosaic **virus**, Pepper huasteco **yellow** vein **virus** and Potato **yellow** mosaic **virus** by 22-48%. electrophoretic mobility shift assays and co-purification studies showed that **Rep**-(1-160) did not bind with high affinity in vitro to the corresponding common region sequences of heterologous geminiviruses. However, **Rep**-(1-160) formed oligomers with the **Rep proteins** of the other geminiviruses. These data suggest that the regulation of **virus** accumulation may involve binding of the **Rep** to target DNA sequences and to the other **Rep** molecules during **virus** replication.

10/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09950307 99036047 PMID: 9820161

Types of variation in DNA-A among isolates of East African cassava mosaic **virus** from Kenya, Malawi and Tanzania.

Zhou X; Robinson DJ; Harrison BD

Scottish Crop Research Institute, Invergowrie, Dundee, UK.

Journal of general virology (ENGLAND) Nov 1998, 79 (Pt 11) p2835-40, ISSN 0022-1317 Journal Code: I9B

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Complete nucleotide sequences of the DNA-A-like molecules of three East African cassava mosaic **virus** (EACMV) isolates from Kenya (-K, 2801 nt) and Malawi (-MH and -MK, both 2804 nt) were determined. These sequences were compared with that published for a Tanzanian isolate (-T, 2801 nt) and the partial sequence of a third Malawian isolate. Intergenic region sequences of all isolates, and deduced amino acid sequences of their AC1 (**Rep**) **proteins**, each formed a tightly related cluster that was distinct from the comparable components of other begomoviruses. Other complementary-sense genes (AC2, AC3, AC4) differed between EACMV isolates in a way consistent with the accumulation of point mutations. In contrast, **virus**-sense genes (CP, AV2) of isolates -MH and -MK differed (substantially for AV2) from those of other EACMV isolates but somewhat resembled those of **tomato yellow leaf curl virus**-Israel, suggesting they had been acquired by recombination with an unidentified begomovirus.

10/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08767922 95249576 PMID: 7732000
In vitro cleavage and joining at the viral origin of replication by the replication initiator **protein** of **tomato yellow leaf curl virus**.
Laufs J; Traut W; Heyraud F; Matzeit V; Rogers SG; Schell J; Gronenborn B
Institut des Sciences Vegetales, Centre National de la Recherche Scientifique, Gif sur Yvette, France.
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Apr 25 1995, 92 (9) p3879-83, ISSN 0027-8424 Journal Code: PV3
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Replication of the single-stranded DNA genome of geminiviruses occurs via a double-stranded intermediate that is subsequently used as a template for rolling-circle replication of the viral strand. Only one of the **proteins** encoded by the **virus**, here referred to as replication initiator **protein** (**Rep protein**), is indispensable for replication. We show that the **Rep protein** of **tomato yellow leaf curl virus** initiates viral-strand DNA synthesis by introducing a nick in the plus strand within the nonanucleotide 1TAATATT decreases 8AC, identical among all geminiviruses. After cleavage, the **Rep protein** remains bound to the 5' end of the cleaved strand. In addition, we show that the **Rep protein** has a joining activity, suggesting that it acts as a terminase, thus resolving the nascent viral single strand into genome-sized units.

10/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08743955 96128241 PMID: 8543063
Identification of the nicking tyrosine of geminivirus **Rep protein**.
Laufs J; Schumacher S; Geisler N; Jupin I; Gronenborn B
Institut des Sciences Vegetales, CNRS, Gif sur Yvette Cedex, France.
FEBS letters (NETHERLANDS) Dec 18 1995, 377 (2) p258-62, ISSN 0014-5793 Journal Code: EUH
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
The replication initiator (**Rep**) **proteins** of geminiviruses perform a DNA cleavage and strand transfer reaction at the viral origin of replication. As a reaction intermediate, **Rep proteins** become covalently linked to the 5' end of the cleaved DNA. We have used **tomato yellow leaf curl virus Rep protein** for in vivo and in vitro analyses. Isolating a covalent peptide-nucleotide complex, we have identified the amino acid of **Rep** which mediates cleavage and links the **protein** to DNA. We show that tyrosine-103, located in a conserved sequence motif, initiates DNA cleavage and is the physical link between geminivirus **Rep protein** and its origin DNA.

10/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08737178 95296367 PMID: 7777563
Rep protein of **tomato yellow leaf curl** geminivirus has an ATPase activity required for viral DNA

replication.
Desbiez C; David C; Mettouchi A; Laufs J; Gronenborn B
Institut des Sciences Vegetales, Centre National de la Recherche Scientifique, Yvette, France.
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Jun 6 1995, 92 (12) p5640-4, ISSN 0027-8424 Journal Code: PV3
Erratum in Proc Natl Acad Sci U S A 1995 Nov 21;92(24) 11322
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
The **Rep protein** of geminiviruses is the sole viral **protein** required for their DNA replication. The amino acid sequence of **Rep protein** contains an NTP binding consensus motif (P-loop). Here we show that purified **Rep protein** of **tomato yellow leaf curl virus** expressed in Escherichia coli exhibits an ATPase activity in vitro. Amino acid exchanges in the P-loop sequence of **Rep** causes a substantial decrease or loss of the ATPase activity. In vivo, mutant **viruses** carrying these **Rep** mutations do not replicate in plant cells. These results show that ATP binding by the **Rep protein** of geminiviruses is required for its function in viral DNA replication.

10/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08735804 95249370 PMID: 7731803
Determination of the origin cleavage and joining domain of geminivirus **Rep proteins**.
Heyraud-Nitschke F; Schumacher S; Laufs J; Schaefer S; Schell J; Gronenborn B
Max-Planck-Institut fur Zuchtungsforschung, Koln, Germany.
Nucleic acids research (ENGLAND) Mar 25 1995, 23 (6) p910-6, ISSN 0305-1048 Journal Code: O8L
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Replication of the single-stranded DNA genome of plant geminiviruses follows a rolling circle mechanism. It strictly depends on a 'rolling circle replication initiator **protein**', the M(r) 41 kDa viral **Rep protein**, encoded by the C1 or AC1 genes. Using wheat dwarf **virus** (WDV) and **tomato yellow leaf curl virus** (TYLCV) as examples, we show that not only the full-size **Rep proteins**, but also a putative 30 kDa translation product of WDV open reading frame C1-N as well as an artificially shortened 24 kDa **Rep** of TYLCV, cleave and join single-stranded origin DNA in vitro. Thus the pivotal origin recognition and processing activities of geminivirus **Rep proteins** must be mediated by the amino-terminal domain of **Rep**.

10/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08735496 95237362 PMID: 7720856
DNA replication specificity of TYLCV geminivirus is mediated by the amino-terminal 116 amino acids of the **Rep protein**.
Jupin I; Hericourt F; Benz B; Gronenborn B
Institut des Sciences Vegetales, CNRS, Gif sur Yvette, France.
FEBS letters (NETHERLANDS) Apr 3 1995, 362 (2) p116-20, ISSN 0014-5793 Journal Code: EUH
Languages: ENGLISH
Document type: Journal Article
Record type: Completed

Geminiviruses are plant DNA **viruses** replicating by a rolling circle mechanism. We have investigated the specificity of replication origin recognition of two different isolates of **tomato yellow leaf curl virus** (TYLCV). Here, we show that TYLCV-Sardinian and -Israeli replication **proteins** display a high degree of specificity for their respective origins. The DNA sequences recognized are located on the left part of the intergenic region whereas the amino-terminal 116 amino acids of the **Rep protein** determine the specificity of origin recognition.

10/3,AB/10 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12991520 BIOSIS NO.: 200100198669
In planta expression of a **protein** encoded by the extrachromosomal DNA of a phytoplasma and related to geminivirus replication **proteins**.
AUTHOR: Nishigawa Hisashi; Miyata Shin-ichi; Oshima Kenro; Sawayanagi Toshimi; Komoto Akihiro; Kuboyama Tsutomu; Matsuda Izumi; Tsuchizaki Tsuneo; Namba Shigetou(a)
AUTHOR ADDRESS: (a)Laboratory of Bioresource Technology, Graduate School of Frontier Sciences, University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo, 113-8657: snamba@ims.u-tokyo.ac.jp**Japan
JOURNAL: Microbiology (Reading) 147 (2):p507-513 February, 2001
MEDIUM: print
ISSN: 1350-0872
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: A new extrachromosomal DNA, EcOYW1, was cloned from the onion yellows phytoplasma (OY-W). Southern blot and PCR analysis showed that EcOYW1 is not present in the OY-M, a mild symptom line derived from OY-W. We determined the complete nucleotide sequence of EcOYW1; it is a circular dsDNA of 7.0 kbp in length, which contains seven ORFs. ORF1 encoded a homologue of the geminivirus **Rep protein**. Western immunoblot analysis revealed that this **Rep** homologue is expressed in OY-W infected plants, suggesting that EcOYW1 replicates via a geminivirus-like rolling-circle replication mechanism. EcOYW1 is the first phytoplasmal extrachromosomal DNA shown to express encoded genes.

2001

10/3,AB/11 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11028346 BIOSIS NO.: 199799649491
High expression of truncated viral **rep protein** confers resistance to **tomato yellow leaf curl virus** in transgenic **tomato** plants.
AUTHOR: Brunetti A; Tavazza M(a); Noris E; Tavazza R; Caciagli P; Ancora G; Crespi S; Accotto G P
AUTHOR ADDRESS: (a)ENEA, Dipartimento Innovazione, C.R. Casaccia, Via Anguillarese 301, 00060 S. Maria di Galeria, **Italy
JOURNAL: Molecular Plant-Microbe Interactions 10 (5):p571-579 1997
ISSN: 0894-0282
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A truncated version of the C1 gene of **tomato yellow leaf curl** geminivirus (TYLCV), encoding the first 210 amino

acids of the multifunc[redacted]nal **Rep protein**, was introduced by Agrobacterium transform[redacted]ion into Lycopersicon esculent[redacted]cv. Moneymaker plants under the transcriptional control of an enhanced cauliflower mosaic **virus** 35S promoter. One R-0 plant (line 47) carrying the C1 gene in two loci (A and B) and accumulating the truncated **Rep protein** (T-**Rep**), was crossed with either a wild-type plant, or a C1 antisense plant (line 10). The wild type (wt) times 47 progeny were phenotypically homogeneous, contained either A or B locus, expressed high levels of T-**Rep protein**, had a "curled" phenotype, and were resistant to TYLCV when challenged either by agroinfection or by the vector Bemisia tabaci. In the 10 times 47 progeny, plants carrying only the sense gene behaved like the wt times 47 progeny, while those containing both sense and antisense transgenes did not accumulate the T-**Rep protein**, showed a normal phenotype, and were not resistant, showing that accumulation of T-**Rep protein** is required to confer TYLCV resistance. Plants accumulating T-**Rep** were susceptible to a distinct geminivirus, **tomato leaf curl virus** (ToLCV-Au).

1997

10/3,AB/12 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10300572 BIOSIS NO.: 199698755490
Geminivirus replication: Analysis of **Rep protein** functions.
AUTHOR: Heyraud-Nitschke F(a); Laufs J; Schumacher S; Schaefer S(a); Schell J(a); Gronenborn B
AUTHOR ADDRESS: (a)Max-Planck-Inst. Zuechtungsforschung, Carl-von-Linne-Weg 10, D-50829 Cologne**Germany
JOURNAL: Agronomie (Paris) 15 (7-8):p497-498 1995
CONFERENCE/MEETING: VIIth Conference on Virus Diseases of Poaceae in Europe Cedex, France May 15-18, 1995
ISSN: 0249-5627
RECORD TYPE: Citation
LANGUAGE: English
1995

10/3,AB/13 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA

3722778 21965216 Holding Library: AGL
Sinaloa **tomato leaf curl** geminivirus: biological and molecular evidence for a new subgroup III **virus**
Idris, A.M. Brown, J.K.
University of Arizona, Tucson.
St. Paul, Minn. : American Phytopathological Society, 1911-
Phytopathology. July 1998. v. 88 (7) p. 648-657.
ISSN: 0031-949X CODEN: PHYTAJ
DNAL CALL NO: 464.8 P56
Language: English
The biological and molecular properties of Sinaloa **tomato leaf curl virus** (STLCV) were investigated in line with the hypothesis that STLCV is a previously uncharacterized, whitefly-transmitted geminivirus from North America. STLCV causes **yellow leaf curl** symptoms in **tomato** and **yellow** -green foliar mottle in pepper. Five species belonging to two plant families were STLCV experimental hosts. STLCV had a persistent relationship with its whitefly vector, Bemisia tabaci. Polymerase chain reaction fragments of STLCV common region (CR) sequences of the A or B genomic components and the viral coat **protein** gene (AV1) were

molecularly cloned and sequenced. The STLCV A- and B-component CR sequences (174 nucleotides each) shared 97.9% identity and contained identical cis elements putatively involved in transcriptional regulation and an origin of replication (the AC cleavage site within the loop of the hairpin structure and two direct repeat sequences thought to constitute the **Rep** binding motif), which collectively are diagnostic for subgroup III geminiviruses. The STLCV CR sequence shared 23.1 to 77.6% identity with CR sequences of representative geminiviridae, indicating the STLCV CR sequence is unique. Molecular phylogenetic analysis of CR or AV1 sequences of STLCV and the respective sequences of 31 familial members supported the placement of STLCV as a unique bipartite, subgroup III **virus** most closely related to other **viruses** from the Western Hemisphere. STLCV is provisionally described as a new species within the genus Begomovirus, family Geminiviridae.

10/3,AB/14 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

09096362 Genuine Article#: 367MC Number of References: 28
Title: Natural recombination between **Tomato yellow leaf curl virus**-Is and **Tomato leaf curl virus** (ABSTRACT AVAILABLE)
Author(s): NavasCastillo J; SanchezCampos S; Noris E; Louro D; Accotto GP; Moriones E (REPRINT)
Corporate Source: CONSEJO SUPER INVEST CIENT,ESTAC EXPT LA MAYORA/MALAGA 29750//SPAIN/ (REPRINT); CONSEJO SUPER INVEST CIENT,ESTAC EXPT LA MAYORA/MALAGA 29750//SPAIN/; CNR,IST FITOVIROL APPLICATA/I-10135 TURIN//ITALY/; DIRECCAO GERAL PROTECCAO CULTURAS,/P-2780 OEIRAS//PORTUGAL/
Journal: JOURNAL OF GENERAL VIROLOGY, 2000, V81, 11 (NOV), P2797-2801
ISSN: 0022-1317 Publication date: 20001100
Publisher: SOC GENERAL MICROBIOLOGY, MARLBOROUGH HOUSE, BASINGSTOKE RD, SPENCERS WOODS, READING RG7 1AE, BERKS, ENGLAND
Language: English Document Type: ARTICLE
Abstract: The complete genome sequences (2791 and 2793 nt) of isolates of **Tomato yellow leaf curl virus**-Is (TYLCV-Is) from Spain (SP72/97) and Portugal (Port2/95) were determined. These isolates are closely related to TYLCV-Is isolates reported in Japan (Japan-A and Japan-S) and Israel (Israel/ Mild). Comparison of all sequenced isolates of TYLCV-Is showed that part of the genome comprising the intergenic region and the 5'-end of the **rep** gene of the Iran and Israel isolates was not closely related to that of other isolates. Phylogenetic analyses suggest that the Israel and Iran isolates may have chimeric genomes that have arisen by recombination between TYLCV-Is-like and **tomato leaf curl virus** (ToLCV)-like ancestors. The TYLCV-Is donors of the Iran and the Israel genomes were closely related to each other and to other known TYLCV-Is isolates. However, the ToLCV donors differed from each other, although both were related to ToLCV isolates from India (Bangalore-2 and Bangalore-4).

10/3,AB/15 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

02537628 4783971
A new geminivirus associated with a **yellow leaf curl** disease of pepper in Thailand
Samretwanich, K.; Chiemsombat, P.; Kittipakorn, K.; Ikegami, M.
Department of Bioscience, Tokyo University of Agriculture, 1-1-1, Sakuragaoka, Setagaya-ku, Tokyo 156-8502, Japan
Plant Disease vol. 84, no. 9, 1047 (2000)

ISSN: 0191-2917
DOCUMENT TYPE: Journal article; Summary LANGUAGE: ENGLISH
SUBFILE: Virology & AIDS Abstracts

Pepper (Capsicum anuum) plants affected with **yellow leaf curl** disease were observed at Kanchanaburi in central Thailand in 1995. Three naturally infected pepper plants showing **yellow leaf curl** were collected and **virus** cultures maintained in pepper plants. Transmission experiments were carried out with the whitefly vector (Bemisia tabaci Genn.). Acquisition and inoculation threshold periods were 1 h and 30 min, respectively. The latent period was 10 h. Symptoms in cultured plants were the same as those observed in field plants. DNA was extracted from these cultured plants and amplified using polymerase chain reaction (PCR) with geminivirus-specific degenerate primers. A PCR product of 2.7 kbp was amplified and cloned. Three independent clones were sequenced and analyzed, and an identical 32-base stem loop region and the unique sequence (TGGGGTC) of putative **Rep** binding site were found in the intergenic region (IR). The B component could not be detected. The nucleotide sequence of the coat **protein** gene was compared with 28 well-studied whitefly-transmitted geminiviruses. Our geminivirus showed the highest sequence similarity (85%) with **Tomato leaf curl virus** from Taiwan (TwToLCV: GeneBank accession number U88692), suggesting that it is a new geminivirus. Therefore, it is designated Pepper **yellow leaf curl virus**.

10/3,AB/16 (Item 2 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

02508976 4744428
Tomato curly stunt **virus**, a New Begomovirus of **Tomato** Within the **Tomato yellow leaf curl virus**-IS Cluster in South Africa
Pietersen, G.; Idris, A.M.; Krueger, K.; Brown, J.K.
ARC-PPRI, Private Bag X134, Pretoria, 0001 South Africa
Plant Disease vol. 84, no. 7, 810 (2000)
ISSN: 0191-2917
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Virology & AIDS Abstracts; Microbiology Abstracts A: Industrial & Applied Microbiology; Entomology Abstracts

Tomato yellow leaf curl virus (TYLCV) causes a serious disease of **tomato** in many countries throughout the world. Preliminary reports suggested that TYLC disease was present in 1997 in South Africa. In 1998 140 ha of **tomato** fields in the Onderberg area were assessed for possible presence of TYLCV. Symptoms like those caused by TYLCV isolates in Israel were observed in most fields, and disease incidence ranged from <1 to 50%. Yield losses in individual plants ranged from negligible to 100% and appeared related to the age of the plants at time of infection. Two isolates of the suspect **virus** were experimentally transmitted from symptomatic **tomato** to **virus** -free, glasshouse-grown **tomato** seedlings by colony. Field and colony whiteflies were identified as the Bemisia tabaci based on mt COI sequence analysis. Attempts to transmit the suspect begomovirus by sap inoculation between **tomato** plants were unsuccessful. Polymerase chain reaction (PCR) amplification with degenerate PCR primers that permit detection of the coat **protein** gene (AV1) and the common region (CR) of other begomoviruses yielded an amplicon of the expected size (2,100 bp), suggesting begomovirus association with diseased **tomato** plants. Nucleotide (nt) sequence analysis of AV1 for both **tomato** isolate AF261885 indicated that they were indistinguishable and shared less than 78% sequence identity with other well-studied begomoviruses, indicating a distinct, previously undescribed begomovirus species. AV1 sequence

comparisons also revealed that its closest relatives were members of the TYLCV cluster, which includes South African cassava mosaic **virus** (77.4%) (AF11785), East African cassava mosaic **virus** (77.3%) (AJ006459), and TYLCV-IS (76.2%) (X15656). The theoretical **Rep** binding element in the CR, TCGGT, was identical to TYLCV-IS and Cotton **leaf curl virus**-Pakistan (AJ002448) (AJ002449). Here, we provisionally designate this new **tomato**-infecting begomoviral species, **Tomato** curly stunt **virus** from South Africa (ToCSV-SA).

10/3,AB/17 (Item 3 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

02498119 4721937
Yellow Leaf Disease of Muskmelon from Thailand Caused by **Tomato leaf curl virus**
Samretwanich, K.; Chiemsombat, P.; Kittipakorn, K.; Ikegami, M.
Department of Bioscience, Tokyo University of Agriculture, 1-1-1, Sakuragaoka, Setagaya-ku, Tokyo
Plant Disease vol. 84, no. 6, p. 707 (2000)
ISSN: 0191-2917
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Virology & AIDS Abstracts; Microbiology Abstracts A: Industrial & Applied Microbiology; Entomology Abstracts

Muskmelon (Cucumis melo L. var. reliculatus) plants exhibiting a **yellow leaf** disease have been observed in central Thailand since 1993. The pathogen is transmitted to muskmelon by the whitefly, Bemisia tabaci Genn. Based on **leaf** yellowing symptoms and whitefly transmission, infection by a geminivirus was suspected. Five naturally infected muskmelon plants showing **leaf** yellowing were collected from a field at Kamphaengsaen, Nakorn Pathom, Thailand, in 1996. **Virus** cultures were maintained in muskmelon plants in a screenhouse. Inoculations were done with B. tabaci, and **leaf** symptoms were the same as symptoms in the field. Geminivirus DNA associated with **yellow leaf** disease of muskmelon was amplified by polymerase chain reaction with geminivirus-specific degenerate primers that anneal within the **rep** (replication-associated **protein**) and cp (coat **protein**) genes. Fragments of 1.2 kb were amplified and cloned from affected muskmelon plants. The insert of three independent clones was sequenced, and identical 32-base stem loop regions were found, including the conserved nonanucleotide sequence TAATAT-TAC present in all geminiviruses. The iterative sequence GGCGTC also was found in the intergenic region (IR 434 bp) of the amplified fragments. The B component was not found from the total length of the restriction fragment sizes of dsDNA isolated from infected muskmelon. The nucleotide sequences of IR and VI (precoat open reading frame) were compared with 28 well-studied whitefly-transmitted geminiviruses and revealed approximately 97% sequence similarity with DNA A of **Tomato leaf curl virus** (genus Geminivirus) from India (ToLCV-In2 GenBank Accession no. u15016). The iterative sequence GGCGTC in the IR also was identical to ToLCV-In2. These results establish the provisional identity of the **virus** causing melon **yellow leaf** disease as ToLCV or closely related strains.

10/3,AB/18 (Item 4 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

02440532 4663977
Association of a Begomovirus and Nanovirus-like Molecule with Ageratum **Yellow** Vein Disease in Pakistan
Mansoor, S.; Khan, S.H.; Hussain, M.; Zafar, Y.; Pinner, M.S.; Briddon, R.W.; Stanley, J.; Markham, P.G.

Plant Biotechnology Division, National Institute for Biotechnology and Genetic Engineering, P.O. Box 577, Faisalabad, Pakistan
Plant Disease vol. 84, no. 1, p.101 (2000)
ISSN: 0191-2917
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Virology & AIDS Abstracts

Whitefly-transmitted geminiviruses (begomoviruses) cause heavy losses to many food and fiber crops in Pakistan. Many weeds also show symptoms typical of begomoviruses. Ageratum (Ageratum conyzoides) is a common perennial weed in Pakistan, growing along irrigation canals, that often shows symptoms, such as **yellow** vein and mosaic, suggesting infection by a begomovirus. To confirm this, symptomatic and asymptomatic ageratum plants were collected from three locations in the Punjab Province of Pakistan, and total DNA was isolated, subjected to agarose gel electrophoresis, transferred to a nylon membrane, and Southern blotted. Total DNA isolated from cotton infected with Cotton **leaf curl virus** (CLCuV), **tomato** infected with **Tomato leaf curl virus** from Pakistan (TLCV-Pak), tobacco infected with African cassava mosaic **virus** (ACMV) from Nigeria, and healthy tobacco were included as controls. A full-length clone of CLCuV DNA A was labeled with super([32P])dCTP by oligo-labeling and hybridized at medium stringency. The probe detected characteristic geminivirus DNA forms in symptomatic ageratum and plants infected with CLCuV, TLCV-Pak, and ACMV, while no signal was detected in asymptomatic ageratum from the field or healthy tobacco. To confirm infection by a begomovirus, degenerate primers WTGF (5'-GATTGTACGCGTCCDCCTTTAATTT GAAYBGG-3'), designed in the **rep** gene of begomoviruses, and WTGR (5'-TANACGCGTGGC TTCKRTACATGGCCTDT-3'), designed in the coat **protein** gene of DNA A of begomoviruses, were used in polymerase chain reaction (PCR). Degenerate primers (PBLv2040 and PCRc1) also were used in PCR. A product of expected size (approximately 1.4 kb) was obtained with DNA A primers from symptomatic ageratum, while no product was obtained with DNA B primers in the same sample. Previously we were unable to detect a DNA component equivalent to begomovirus DNA B in cotton showing symptoms of cotton **leaf curl** disease. We recently reported a novel circular DNA molecule that was approximately half as long as the full-length DNA A (CLCuV DNA-1) associated with CLCuV that share homology to plant nanoviruses. The supercoiled replicative form of viral DNA isolated from infected ageratum plants indicated the presence of smaller molecules, as was found in cotton **leaf curl** disease, suggesting that a nanovirus-like molecule might be associated with ageratum **yellow** vein disease. A duplicate blot of samples used in Southern hybridization with the DNA A probe was prepared, and a probe of the full-length clone of the nanovirus-like molecule (CLCuV DNA-1) was prepared as described for DNA A. The probe detected characteristic nanovirus DNA forms in ageratum with **yellow** vein symptoms and cotton infected with CLCuV, while no signal was detected in plants infected with TLCV-Pak or ACMV, healthy tobacco, or asymptomatic ageratum. Abutting primers PB2-F and PB2R, designed based on the CLCuV DNA-1 sequence, were unable to amplify a PCR product from ageratum with **yellow** vein symptoms, suggesting the nanovirus-like molecule associated with ageratum **yellow** vein disease is distinct from CLCuV DNA-1. Our results show that **yellow** vein disease of ageratum in Pakistan is associated with a begomovirus infection and single-stranded circular DNA molecule with similarity to CLCuV DNA-1.

10/3,AB/19 (Item 5 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

01908757 3721705
Determination of the origin cleavage and joining domain of geminivirus **Rep proteins**
Heyraud Nitschke, F.; Schumacher, S.; Laufs, J.; Schaefer, S.; Schell, J.; Gronenborn, B.

Max-Planck-Inst. Zuechtu[redacted]forsch., Carl-von-Linne-Weg 10, D-50829 Koeln, FRG
NUCLEIC ACIDS RES. vol. 23, no. 6, pp. 910-916 (1995)
ISSN: 0305-1048
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Virology & AIDS Abstracts; Biochemistry Abstracts 2: Nucleic Acids

Replication of the single-stranded DNA genome of plant geminiviruses follows a rolling circle mechanism. It strictly depends on a "rolling circle replication initiator **protein**", the M sub(r) 41 kDa viral **Rep protein**, encoded by the C1 or AC1 genes. Using wheat dwarf **virus** (WDV) and **tomato yellow leaf curl virus** (TYLCV) as examples, we show that not only the full-size **Rep proteins**, but also a putative 30 kDa translation product of WDV open reading frame C1-N as well as an artificially shortened 24 kDa **Rep** of TYLCV, cleave and join single-stranded origin DNA in vitro. Thus the pivotal origin recognition and processing activities of geminivirus **Rep proteins** must be mediated by the amino-terminal domain of **Rep**.

10/3,AB/20 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

13254084 PASCAL No.: 97-0524296
Structure et fonction de deux **proteines** impliquees dans la replication de l'ADN: la **proteine Rep** du geminivirus de jaunissement et de l'enroulement de feuille de tomate (TYLCV) et la transposase du phage Mu
(Structure and function of two **proteins** involved in DNA replication: **Tomato yellow leaf curl** geminivirus **Rep protein** and phage Mu transposase)
SCHUMACHER Silke; GRONENBORN B, dir
Universite de Paris 11, Orsay, Francee
Univ.: Universite de Paris 11. Orsay. FRA Degree: Th. doct.
1997-01; 1997 170 p.
Language: French Summary Language: French; English
La **proteine Rep** d'un geminivirus et la transposase du phage Mu ont ete etudiees comme modeles de **proteines** virales impliquees dans la replication de l'ADN viral. Les geminivirus sont des **virus** de plantes. Leur petit genome d'ADN simple brin code entre autres pour la **proteine** virale multifonctionnelle essentielle a la replication **Rep** . L'activite de clivage de l'ADN et de transfert de nucleotide a ete localisee dans les 120 residus de la partie amino-terminale de la **proteine Rep** du TYLCV ou **virus** du jaunissement et de l'enroulement des feuilles de la tomate. In vitro, la presence de magnesium est requise pour l'etape de clivage et de transfert de nucleotide au niveau de l'origine de replication de l'ADN viral. La substitution du magnesium par du manganese ne modifie pas l'activite normale de la **proteine Rep** , la presence de barium l'abolit. Apres l'etape de clivage, l'extremite 5' de l'ADN viral est liee de facon covalente au residu tyrosine 103 de la **proteine Rep**. Lorsque le residu tyrosine 103 est remplace par un residu phenylalanine, l'activite de clivage de l'ADN et de transfert de nucleotide est abolie. La transposase MuA est indispensable a la transposition precedant la replication du phage Mu. Pendant la transposition, MuA s'associe avec les sequences d'ADN donneur et accepteur pour former des complexes nucleoproteiques d'ordre superieur. L'assemblage de ces complexes necessite l'attachement du domaine terminal de MuA aux extremites du genome de Mu. Le domaine terminal de MuA (I beta gamma , residus 77 a 247) peut etre divise en deux sous-domaines de repliement, I beta et I gamma , comprenant respectivement les residus 77 a 174 et 174 a 247. La structure en solution du sous-domaine I gamma a ete determinee par spectroscopie RMN multidimensionnelle et heteronucleaire. Ce domaine contient une structure en faisceau helicoidal semblable a celle rencontree

chez d'autres recombinases et chez un homeodomaine eucaryote. La structure en solution du sous-domaine I beta contient un motif helice-tour-helice dont la structure est similaire a l'aporepresseur trp. Par analyse biochimique, il est propose que la haute affinite du domaine I beta gamma de MuA pour l'ADN est mediee par une interaction directe du sous-domaine I beta avec la moitie 3' d'un site d'association de 22 pb. L'affinite du sous-domaine I beta est augmentee en presence du sous-domaine I gamma par effet cooperatif

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? s rep and protein?
Processing
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        6203960  PROTEIN?
      S1    4853  REP AND PROTEIN?
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Processing
Processing
Processed  10 of  20 files ...
Processing
Processed  20 of  20 files ...
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        7829156  PLANT?
        2587381  RESIST?
        3920475  INHIBIT?
      S2      87  S1 AND VIRUS? AND PLANT? AND (RESIST? OR INHIBIT?)
? rd
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>>>Records from unsupported files will be retained in the RD set.
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>>>Record 266:275036 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:272648 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:269993 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:263053 ignored; incomplete bibliographic data, not retained -
in RD set
>>>Record 266:260573 ignored; incomplete bibliographic data, not retained -
in RD set
...completed examining records
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>>>No matching display code(s) found in file(s): 65, 306

 3/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11533964   21326165   PMID: 11342533
   Expression  of  the oligomerization domain of the replication-associated
protein  (Rep)  of  Tomato  leaf  curl  New  Delhi  virus
 interferes with DNA accumulation of heterologous geminiviruses.
  Chatterji A; Beachy RN; Fauquet CM
  International  Laboratory for Tropical Agricultural Biotechnology, Donald
Danforth  Plant  Science  Center,  8001  Natural Bridge Road, St. Louis, MO
63121, USA.
  Journal  of biological chemistry (United States)   Jul 6 2001,  276  (27)
 p25631-8,  ISSN 0021-9258   Journal Code: HIV
  Languages: ENGLISH
```

Document type: Journal Article
Record type: Completed
The minimal DNA binding domain of the replication-associated **protein** (**Rep**) of Tomato leaf curl New Delhi **virus** was determined by electrophoretic mobility gel shift analysis and co-purification assays. DNA binding activity maps to amino acids 1-160 (**Rep**-(1-160)) of the **Rep protein** and overlaps with the **protein** oligomerization domain. Transient expression of **Rep protein** (**Rep**-(1-160)) was found to **inhibit** homologous viral DNA accumulation by 70-86% in tobacco protoplasts and in Nicotiana benthamiana **plants** . The results obtained showed that expression of N-terminal sequences of **Rep protein** could efficiently interfere with DNA binding and oligomerization activities during **virus** infection. Surprisingly, this **protein** reduced accumulation of the African cassava mosaic **virus**, Pepper huasteco yellow vein **virus** and Potato yellow mosaic **virus** by 22-48%. electrophoretic mobility shift assays and co-purification studies showed that **Rep**-(1-160) did not bind with high affinity in vitro to the corresponding common region sequences of heterologous geminiviruses. However, **Rep**-(1-160) formed oligomers with the **Rep proteins** of the other geminiviruses. These data suggest that the regulation of **virus** accumulation may involve binding of the **Rep** to target DNA sequences and to the other **Rep** molecules during **virus** replication.

3/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10579001 20256475 PMID: 10798617
Secreted **proteins** of tobacco cultured BY2 cells: identification of a new member of pathogenesis-related **proteins**.
Okushima Y; Koizumi N; Kusano T; Sano H
Research and Education Center for Genetic Information, Nara Institute of Science and Technology, Ikoma, Japan.
Plant molecular biology (NETHERLANDS) Feb 2000, 42 (3) p479-88, ISSN 0167-4412 Journal Code: A6O
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Cultured cells of tobacco BY2 secrete more than 100 **proteins** into culture medium. Six major **proteins** were purified, and partial **protein** sequences were determined. Five of them were found to be similar to an ascorbic acid oxidase, three peroxidase isozymes and a beta-1,3-exoglucanase, respectively. A cDNA clone encoding the remaining polypeptide, whose amino acid sequence showed no similarity with earlier reported **proteins**, was isolated. It encoded a putative 27 kDa **protein** of 242 amino acids with resemblance to WCI-5, a wheat **protein** induced by benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester (BTH) which activates genes involved in systemic acquired **resistance**. Transcripts of this clone accumulated upon tobacco mosaic **virus** infection, mechanical wounding and drought treatment, an induction profile that satisfies the definition of pathogenesis-related (PR) **proteins** by van Loon et al. (**Plant** Mol. Biol. **Rep**. 12 (1994) 245). No similar PR **proteins** have so far been reported, and therefore our newly designated NtPRp27 points to the existence of a novel PR **protein** family in tobacco **plants**.

3/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10534555 20158912 PMID: 10692401
The multifunctional character of a geminivirus replication **protein** is reflected by its complex oligomerization properties.
Orozco BM; Kong LJ; Batts LA; Elledge S; Hanley-Bowdoin L

Department of Biochemistry, North Carolina State University, Raleigh, North Carolina 27695-762[redacted] USA.
Journal of biological chemistry (UNITED STATES) Mar [redacted] 2000, 275 (9) p6114-22, ISSN 0021-9258 Journal Code: HIV
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Tomato golden mosaic **virus** (TGMV), a member of the geminivirus family, encodes one essential replication **protein**, AL1, and recruits the rest of the DNA replication apparatus from its **plant** host. TGMV AL1 is an oligomeric **protein** that binds double-stranded DNA and catalyzes cleavage and ligation of single-stranded DNA. The oligomerization domain, which is required for DNA binding, maps to a region that displays strong sequence and structural homology to other geminivirus **Rep proteins** . To assess the importance of conserved residues, we generated a series of site-directed mutations and analyzed their impact on AL1 function in vitro and in vivo. Two-hybrid experiments revealed that mutation of amino acids 157-159 **inhibited** AL1-AL1 interactions, whereas mutations at nearby residues reduced complex stability. Changes at positions 157-159 also disrupted interaction between the full-length mutant **protein** and a glutathione S-transferase-AL1 oligomerization domain fusion in insect cells. The mutations had no detectable effect on oligomerization when both **proteins** contained full-length AL1 sequences, indicating that AL1 complexes can be stabilized by amino acids outside of the oligomerization domain. Nearly all of the oligomerization domain mutants were **inhibited** or severely attenuated in their ability to support AL1-directed viral DNA replication. In contrast, the same mutants were enhanced for AL1-mediated transcriptional repression. The replication-defective AL1 mutants also interfered with replication of a TGMV A DNA encoding wild type AL1. Full-length mutant AL1 was more effective in the interference assays than truncated **proteins** containing the oligomerization domain. Together, these results suggested that different AL1 complexes mediate viral replication and transcriptional regulation and that replication interference involves multiple domains of the AL1 **protein**.

3/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10146445 99277583 PMID: 10350080

GRAB **proteins**, novel members of the NAC domain family, isolated by their interaction with a geminivirus **protein**.

Xie Q; Sanz-Burgos AP; Guo H; Garcia JA; Gutierrez C
Centro de Biologia Molecular 'Severo Ochoa' (CSIC-UAM), Universidad Autonoma, Madrid, Spain.
Plant molecular biology (NETHERLANDS) Mar 1999, 39 (4) p647-56, ISSN 0167-4412 Journal Code: A6O
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Geminiviruses encode a few **proteins** and depend on cellular factors to complete their replicative cycle. As a way to understand geminivirus-host interactions, we have searched for cellular **proteins** which interact with viral **proteins**. By using the yeast two-hybrid technology and the wheat dwarf geminivirus (WDV) RepA **protein** as a bait, we have isolated a family of **proteins** which we termed GRAB (for Geminivirus **Rep** A-binding). We report here the molecular characterization of two members, GRAB1 and GRAB2. We have found that the 37 C-terminal amino acids of RepA are required for interaction with GRAB **proteins** . This region contains residues conserved in an equivalent region of the RepA **proteins** encoded by other **viruses** of the WDV subgroup. The N-terminal domain of GRAB **proteins** is necessary and sufficient to interact with WDV RepA. GRAB **proteins** contain an unique acidic C-terminal domain while their N-terminal domain, of ca. 170 amino

acids, are highly conserved in all of them. Interestingly, this conserved N-terminal domain of GRAB **proteins** exhibits a significant amino acid homology to the NAC domain present in **proteins** involved in **plant** development and senescence. GRAB1 and GRAB2 mRNAs are present in cultured cells and roots but are barely detectable in leaves. GRAB expression **inhibits** WDV DNA replication in cultured wheat cells. Our studies highlight the importance that the pathway(s) mediated by GRAB **proteins**, as well as by other NAC domain-containing **proteins**, might have on geminivirus DNA replication in connection to **plant** growth, development and senescence pathways.

3/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09266302 97188567 PMID: 9037152
Engineering **resistance** against tomato yellow leaf curl **virus** (TYLCV) using antisense RNA.
Bendahmane M; Gronenborn B
Centre National de la Recherche Scientifique, Gif-sur-Yvette, France.
Plant molecular biology (NETHERLANDS) Jan 1997, 33 (2) p351-7, ISSN 0167-4412 Journal Code: A6O
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
One of the most severe diseases of cultivated tomato worldwide is caused by tomato yellow leaf curl **virus** (TYLCV), a geminivirus transmitted by the whitefly Bemisia tabaci. Here we describe the application of antisense RNAs to interfere with the disease caused by TYLCV. The target of the antisense RNA is the rare messenger RNA of the **Rep protein**, encoded by the C1 gene. Transgenic Nicotiana benthamiana **plants** expressing C1 antisense RNA were obtained and shown to **resist** infection by TYLCV. Some of the **resistant** lines are symptomless, and the replication of challenge TYLCV almost completely suppressed. The transgenes mediating **resistance** were shown to be effective through at least two generations of progeny.

3/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09018873 97015759 PMID: 8862407
Resistance to tomato yellow leaf curl geminivirus in Nicotiana benthamiana **plants** transformed with a truncated viral C1 gene.
Noris E; Accotto GP; Tavazza R; Brunetti A; Crespi S; Tavazza M
Istituto di Fitovirologia Applicata, National Research Council, Turin, Italy.
Virology (UNITED STATES) Oct 1 1996, 224 (1) p130-8, ISSN 0042-6822 Journal Code: XEA
Erratum in Virology 1997 Jan 20;227(2) 519
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
The C1 gene of tomato yellow leaf curl geminivirus (TYLCV) encodes a multifunctional **protein** (**Rep**) involved in replication. A truncated form of this gene, capable of expressing the N-terminal 210 amino acids (aa) of the **Rep protein**, was cloned under the control of the CaMV 35S promoter and introduced into Nicotiana benthamiana using Agrobacterium tumefaciens. The same sequence was also cloned in antisense orientation. When self-pollinated progeny of 19 primary transformants were tested for **resistance** to TYLCV by agroinoculation, some **plants** proved to be **resistant**, particularly in the sense lines. Two such lines were further studied. The presence of the transgene was verified and its expression was followed at intervals. All **plants** that were **resistant** to TYLCV at 4 weeks postinoculation (wpi) contained

detectable amounts of transgenic mRNA and **protein** at the time of infection. **Resistance** [redacted] overcome in a few **plants** at [redacted] wpi, and in most at 15 wpi. Infection of leaf discs derived from transgenic **plants** showed that expression of the transgene correlated with a substantial reduction of viral DNA replication. Cotransfections of tobacco protoplasts demonstrated that **inhibition** of viral DNA replication requires expression of the truncated **Rep protein** and suggested that the small ORF C4, also present in our construct, plays no role in the **resistance** observed. The results obtained using both transient and stable gene expression systems show that the expression of the N-terminal 210 aa of the TYLCV **Rep protein** efficiently interferes with **virus** infection.

3/3,AB/7 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12593275 BIOSIS NO.: 200000346777
Characterization of a phage **resistance** plasmid, pLKS, of silage-making Lactobacillus **plantarum** NGRI0101.
AUTHOR: Eguchi Tomoko; Doi Katsumi; Nishiyama Kanako; Ohmomo Sadahiro; Ogata Seiya(a)
AUTHOR ADDRESS: (a)Microbial Genetics Division, Faculty of Agriculture, Institute of Genetic Resources, Kyushu University, Hakozaki, Fukuoka, 812-8581**Japan
JOURNAL: Bioscience Biotechnology and Biochemistry 64 (4):p751-756 April, 2000
MEDIUM: print
ISSN: 0916-8451
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Phage contamination has resulted in abnormal fermentation in silage. We isolated a phage-**resistant** strain, Lactobacillus **plantarum** NGRI0101 from silage. The strain carried two plasmids, pLKL (6.8 kb) and pLKS (2.0 kb). By curing and retransformation of the plasmids, we clarified that pLKS has phage **resistant** activity, characterized as no adsorption **inhibition**. pLKS has 2,025 bp and three orfs, orf123, orf132, and orf918. The predicted amino acid sequence of the orf918 product showed high similarity to those of **Rep proteins** of Pediococcus halophilus plasmid pUCL287 and Lactobacillus acidophilus plasmid pLA103. The replication origin (ori) was upstream from orf918. There was no gene similar to typical phage **resistant** genes encoded by known plasmids. The phage **resistance** of L. **plantarum** NGRI0101 may possibly be due to a plasmid-encoded abortive infection.

2000

3/3,AB/8 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12235884 BIOSIS NO.: 199900530733
Near immunity to rice tungro spherical **virus** achieved in rice by a replicase-mediated **resistance** strategy.
AUTHOR: Huet H; Mahendra S; Wang J; Sivamani E; Ong C A; Chen L; de Kochko A(a); Beachy R N; Fauquet C(a)
AUTHOR ADDRESS: (a)ILTAB, (IRD-DPSC), TSRI, CAL7, 10550 N. Torrey Pines Road, La Jolla, CA, 92037**USA
JOURNAL: Phytopathology 89 (11):p1022-1027 Nov., 1999

ISSN: 0031-949X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Rice tungro disease is caused by rice tungro bacilliform **virus** (RTBV), which is responsible for the symptoms, and rice tungro spherical **virus** (RTSV), which assists transmission of both **viruses** by leafhoppers. Transgenic japonica rice **plants** (Oryza sativa) were produced containing the RTSV replicase (**Rep**) gene in the sense or antisense orientation. Over 70% of the **plants** contained one to five copies of the **Rep** gene, with integration occurring at a single locus in most cases. **Plants** producing antisense sequences exhibited significant but moderate **resistance** to RTSV (60%); accumulation of antisense RNA was substantial, indicating that the protection was not of the homology-dependent type. **Plants** expressing the full-length **Rep** gene, as well as a truncated **Rep** gene, in the (+)- sense orientation were 100% **resistant** to RTSV even when challenged with a high level of inoculum. Accumulation of viral RNA was low, leading us to conclude that RTSV **Rep**-mediated **resistance** is not **protein**-mediatedbut is of the cosuppression type. **Resistance** was effective against geographically distinct RTSV isolates. In addition, RTSV-**resistant** transgenic rice **plants** were unable to assist transmission of RTBV. Such transgenic **plants** could be used in an epidemiological approach to combat the spread of the tungro disease.

1999

3/3,AB/9 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11028346 BIOSIS NO.: 199799649491
High expression of truncated viral **rep protein** confers **resistance** to tomato yellow leaf curl **virus** in transgenic tomato **plants**.
AUTHOR: Brunetti A; Tavazza M(a); Noris E; Tavazza R; Caciagli P; Ancora G; Crespi S; Accotto G P
AUTHOR ADDRESS: (a)ENEA, Dipartimento Innovazione, C.R. Casaccia, Via Anguillarese 301, 00060 S. Maria di Galeria, **Italy
JOURNAL: Molecular Plant-Microbe Interactions 10 (5):p571-579 1997
ISSN: 0894-0282
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A truncated version of the C1 gene of tomato yellow leaf curl geminivirus (TYLCV), encoding the first 210 amino acids of the multifunctional **Rep protein**, was introduced by Agrobacterium transformation into Lycopersicon esculentum cv. Moneymaker **plants** under the transcriptional control of an enhanced cauliflower mosaic **virus** 35S promoter. One R-0 **plant** (line 47) carrying the C1 gene in two loci (A and B) and accumulating the truncated **Rep protein** (T-**Rep**), was crossed with either a wild-type **plant**, or a C1 antisense **plant** (line 10). The wild type (wt) times 47 progeny were phenotypically homogeneous, contained either A or B locus, expressed high levels of T-**Rep protein**, had a "curled" phenotype, and were **resistant** to TYLCV when challenged either by agroinfection or by the vector Bemisia tabaci. In the 10 times 47 progeny, **plants** carrying only the sense gene behaved like the wt times 47 progeny, while those containing both sense and antisense transgenes did not accumulate the T-**Rep protein**, showed a normal phenotype, and were not **resistant**, showing that accumulation

of T-**Rep protein** is required to confer TYLCV **resistance**. **Plants** accumulating **Rep** were susceptible to a distinct geminivirus, tomato leaf curl **virus** (ToLCV-Au).

1997

3/3,AB/10 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA

3785219 22011357 Holding Library: AGL
GRAB **proteins**, novel membranes of the NAC domain family, isolated by their interaction with a geminivirus **protein**
Xie, Q. Sanz-Burgos, A.P.; Guo, H.S.; Garcia, J.A.; Gutierrez, C.
CSIC-UAM, Madrid, Spain.
Dordrecht : Kluwer Academic Publishers.
Plant molecular biology. Mar 1999. v. 39 (4) p. 647-656.
ISSN: 0167-4412 CODEN: PMBIDB
DNAL CALL NO: QK710.P62
Language: English
Geminiviruses encode a few **proteins** and depend on cellular factors to complete their replicative cycle. As a way to understand geminivirus-host interactions, we have searched for cellular **proteins** which interact with viral **proteins**. By using the yeast two-hybrid technology and the wheat dwarf geminivirus (WDV) RepA **protein** as a bait, we have isolated a family of **proteins** which we termed GRAB (for Geminivirus **Rep** A-binding). We report here the molecular characterization of two members, GRAB1 and GRAB2. We have found that the 37 C-terminal amino acids of RepA are required for interaction with GRAB **proteins**. This region contains residues conserved in an equivalent region of the RepA **proteins** encoded by other **viruses** of the WDV subgroup. The N-terminal domain of GRAB **proteins** is necessary and sufficient to interact with WDV RepA. GRAB **proteins** contain an unique acidic C-terminal domain while their N-terminal domain, of ca. 170 amino acids, are highly conserved in all of them. Interestingly, this conserved N-terminal domain of GRAB **proteins** exhibits a significant amino acid homology to the NAC domain present in **proteins** involved in **plant** development and senescence. GRAB1 and GRAB2 mRNAs are present in cultured cells and roots but are barely detectable in leaves. GRAB expression **inhibits** WDV DNA replication in cultured wheat cells. Our studies highlight the importance that the pathway(s) mediated by GRAB **proteins**, as well as by other NAC domain-containing **proteins**, might have on geminivirus DNA replication in connection to **plant** growth, development and senescence pathways.

3/3,AB/11 (Item 2 from file: 10)
DIALOG(R)File 10:AGRICOLA

3774019 21995688 Holding Library: AGL
A search for evidence of **virus**/transgene interactions in potatoes transformed with the potato leafroll **virus** replicase and coat **protein** genes
Thomas, P.E. Hassan, S.; Kaniewski, W.K.; Lawson, E.C.; Zalewski, J.C.
Vegetable and Forage Crop Production, ARS, USDA, Prosser, WA.
Dordrecht ; Boston : Kluwer Academic Publishers, c1995-
Molecular breeding : new strategies in plant improvement. Oct 1998. v. 4 (5) p. 407-417.
ISSN: 1380-3743 CODEN: MOBRFL
DNAL CALL NO: QK981.4.M63
Language: English
A search was conducted to detect evidence for interactions between potato leafroll **virus** (PLRV)-derived transgenes expressed in Russet Burbank

potato and **viruses** to which the transgenic **plants** were exposed and by which they were infected. More than 25000 **plants** in 442 lines transformed with 16 different coat **protein** gene (CP) constructs and nearly 40000 **plants** in 512 lines transformed with seven different replicase gene (**Rep**) constructs of PLRV were exposed to field infection over a 6-year period. These **plants** were individually inspected for type and severity of **virus** symptoms. Heterologous **viruses** found infecting the **plants** were identified and examined for alterations in transmission characteristics, serological affinity, host range, and symptoms. Selected isolates of PLRV from field-infected **plants** were examined for unusual symptoms produced in diagnostic hosts and for alteration in sedimentation properties in density gradient tubes. **Viruses** that were propagated in selected transgenic lines in a greenhouse were examined for similar alterations. Transmission characteristics and serological properties were not altered when they replicated in potatoes containing CP constructs in the field or greenhouse. Potato **plants** expressing CP or **Rep** constructs of PLRV were not infected in the field or in the greenhouse with **viruses** that do not normally infect potato. New **viruses** or **viruses** with altered sedimentation characteristics, symptoms, or host range were not detected in field-exposed or greenhouse-inoculated potato **plants** expressing CP or **Rep** gene constructs of PLRV.

3/3,AB/12 (Item 3 from file: 10)
DIALOG(R)File 10:AGRICOLA

3767221 21995664 Holding Library: AGL

Resistance to African cassava mosaic **virus** conferred by a mutant of the putative NTP-binding domain of the **Rep** gene (AC1) in Nicotiana benthamiana

Sangare, A. Deng, D.; Fauquet, C.M.; Beachy, R.N.
Universite de Cocody, Abidjan, Ivory Coast.

Dordrecht ; Boston : Kluwer Academic Publishers, c1995-
Molecular breeding : new strategies in plant improvement. 1999. v. 5 (2) p. 95-102.
ISSN: 1380-3743 CODEN: MOBRFL
DNAL CALL NO: QK981.4.M63
Language: English

We constructed a mutation in african cassava mosaic **virus** (ACMV) to alter the putative NTP-binding site in the replication-associated **protein** gene (AC1). When transgenic Nicotiana benthamiana **plants** expressing the mutated AC1 gene were infected with ACMV, the **plants** exhibited tolerance to infection consisting in a delay in symptom appearance and/or the presence of mild symptoms. In addition, the **resistant plants** accumulated less viral DNA than non-transgenic **plants** . As judged by northern blot analysis and symptom development of segregating progeny from different lines, a high level of expression of the mutated AC1 gene is essential for the development of **resistance**. Issues related to the use of different versions of AC1 for the control of ACMV are discussed.

3/3,AB/13 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

08668408 Genuine Article#: 314FV Number of References: 53
Title: Differential regulation of plastidial and cytosolic isoforms of peptide methionine sulfoxide reductase in Arabidopsis (ABSTRACT AVAILABLE)
Author(s): Sadanandom A; Poghosyan Z; Fairbairn DJ; Murphy DJ (REPRINT)
Corporate Source: JOHN INNES CTR PLANT SCI RES,DEPT BRASSICA & OILSEEDS RES, NORWICH RES PK/NORWICH NR4 7UH/NORFOLK/ENGLAND/ (REPRINT); JOHN

INNES CTR PLANT SCI RES,DEPT BRASSICA & OILSEEDS RES/NORWICH NR4 7UH/NORFOLK/ENGLAND/
Journal: PLANT PHYSIOLOGY, 2000, V123, N1 (MAY), P255-263
ISSN: 0032-0889 Publication date: 20000500
Publisher: AMER SOC PLANT PHYSIOLOGISTS, 15501 MONONA DRIVE, ROCKVILLE, MD 20855
Language: English Document Type: ARTICLE
Abstract: We report the characterization of two members of a gene family from Arabidopsis that encode, respectively, cytosolic (cPMSR) and plastid-targe ted (pPMSR) isoforms of the oxidative-stress-**rep** air enzyme peptide methionine sulfoxide reductase. Overexpression of these **proteins** in Escherichia coli confirmed that each had PMSR enzyme activity with a synthetic substrate, N-acetyl-[H-3]-methionine sulfoxide, or a biological substrate, alpha-1 **proteinase inhibitor**. The pPMSR was imported into intact chloroplasts in vitro with concomitant cleavage of its approximately 5-kD N-terminal signal peptide. The two PMSR isoforms exhibited divergent pH optima, tissue localization, and responses to developmental and environmental effects. Analysis of the Arabidopsis database indicated that there are probably at least two p-pmsr-like genes and three c-pmsr-like genes in the Arabidopsis genome. Expression of the p-pmsr genes and their **protein** products was restricted to photosynthetic tissues and was strongly induced following illumination of etiolated seedlings. In contrast, the c-pmsr genes were expressed at moderate levels in all tissues and were only weakly affected by light. Exposure to a variety of biotic and abiotic stresses showed relatively little effect on pmsr gene expression, with the exception of leaves subjected to a long-term exposure to the cauliflower mosaic **virus**. These leaves showed a strong induction of the c-pmsr gene after 2 to 3 weeks of chronic pathogen infection. These data suggest novel roles for PMSR in photosynthetic tissues and in pathogen defense responses in **plants**.

3/3,AB/14 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

07707689 Genuine Article#: 198XF Number of References: 48
Title: trans-dominant **inhibition** of geminiviral DNA replication by bean golden mosaic geminivirus **rep** gene mutants (ABSTRACT AVAILABLE)
Author(s): Hanson SF (REPRINT) ; Maxwell DP
Corporate Source: UNIV WISCONSIN,DEPT PLANT PATHOL/MADISON//WI/53706 (REPRINT)
Journal: PHYTOPATHOLOGY, 1999, V89, N6 (JUN), P480-486
ISSN: 0031-949X Publication date: 19990600
Publisher: AMER PHYTOPATHOLOGICAL SOC, 3340 PILOT KNOB ROAD, ST PAUL, MN 55121
Language: English Document Type: ARTICLE
Abstract: Geminiviruses are a group of single-stranded DNA **viruses** that cause major losses on a number of important crops throughout the world. Bean golden mosaic **virus** (BGMV) is a typical bipartite, whitefly-transmitted geminivirus that causes a severe disease on beans (Phaseolus vulgaris) in the Western Hemisphere. The lack of natural **resistance** to geminiviruses has led to attempts to engineer **resistance**, particularly through the use of pathogen-derived **resistance** strategies. The **rep** gene contains several conserved domains including nucleoside triphosphate (NTP)-binding and DNA-nicking domains and is the only geminiviral gene necessary for replication. Previous analysis by our group and others has demonstrated that the NTP-binding and DNA-nicking domains are necessary for geminiviral DNA replication. The ability of the **rep** gene and **rep** gene mutants to interfere with geminiviral DNA replication, when expressed in trans, was examined using a transient assay in a

tobacco suspension cell culture system. Wild-type (wt) and mutant **rep** genes were cloned into plasmids under the control of the cauliflower mosaic **virus** 35S promoter for in **planta** expression and coinoculated into tobacco cells with infectious clones of various geminiviruses. The wt **rep** gene from BGMV-GA was able to support replication of BGMV-GA DNA-B. Several different **rep** gene mutants, with function-abolishing mutations in the NTP-binding or DNA-nicking domains, were potent trans-dominant **inhibitors** of geminiviral DNA replication.

3/3,AB/15 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

07365239 Genuine Article#: 156GE Number of References: 34
Title: Transgenic beans (Phaseolus vulgaris L.) engineered to express viral antisense RNAs show delayed and attenuated symptoms to bean golden mosaic geminivirus (ABSTRACT AVAILABLE)
Author(s): Aragao FJL (REPRINT) ; Ribeiro SG; Barros LMG; Brasileiro ACM; Maxwell DP; Rech EL; Faria JC
Corporate Source: CENARGEN,EMBRAPA, CAIXA POSTAL 02372/BR-70840970 BRASILIA/DF/BRAZIL/ (REPRINT); UNIV WISCONSIN,DEPT PLANT PATHOL/MADISON//WI/53706; CNPAF,EMBRAPA/BR-74001970 GOIANIA/GO/BRAZIL/
Journal: MOLECULAR BREEDING, 1998, V4, N6, P491-499
ISSN: 1380-3743 Publication date: 19980000
Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: The genes **Rep**-TrAP-REn and BC1 from the Brazilian isolate bean golden mosaic geminivirus (BGMV-BR) were cloned in antisense orientation under the transcriptional control of the CaMV 35S promoter. This construct was used to transform common bean (Plaseolus vulgaris L.) using the biolistic method. Transgenic **plants** from the R-3 and R-4 generations were challenged by inoculation with a BGMV-BR viruliferous whitefly population. Of the four transgenic lines tested, two had both delayed and attenuated viral symptoms. Un-transformed **plants** or **plants** transformed with a construct containing only the gus-neo gene developed typical BGMV-BR symptoms 10-15 days after inoculation.

3/3,AB/16 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05059498 Genuine Article#: TM328 Number of References: 50
Title: IDENTIFICATION OF THE NICKING TYROSINE OF GEMINIVIRUS **REP PROTEIN** (Abstract Available)
Author(s): LAUFS J; SCHUMACHER S; GEISLER N; JUPIN I; GRONENBORN B
Corporate Source: CNRS,INST SCI VEGETALES,AVE TERRASSE/F-91198 GIF SUR YVETTE//FRANCE/; CNRS,INST SCI VEGETALES/F-91198 GIF SUR YVETTE//FRANCE/; NIDDK,PHYS CHEM LAB/BETHESDA//MD/20892; MAX PLANCK INST BIOPHYS CHEM/D-37077 GOTTINGEN//GERMANY/
Journal: FEBS LETTERS, 1995, V377, N2 (DEC 18), P258-262
ISSN: 0014-5793
Language: ENGLISH Document Type: ARTICLE
Abstract: The replication initiator (**Rep**) **proteins** of geminiviruses perform a DNA cleavage and strand transfer reaction at the viral origin of replication, As a reaction intermediate, **Rep proteins** become covalently linked to the 5' end of the cleaved DNA, We have used tomato yellow leaf curl **virus Rep protein** for in vivo and in vitro analyses, Isolating a covalent peptide-nucleotide complex, we have identified the amino acid of **Rep** which mediates cleavage and links the **protein** to DNA,

We show that tyrosine 103, located in a conserved sequence motif, initiates DNA cleava[redacted]and is the physical link betwe[redacted]geminivirus **Rep protein** and its origin DNA.

3/3,AB/17 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts

04006233 CAB Accession Number: 20003018685
Genome organization, variability and control of Faba bean necrotic yellows **virus**, a nanovirus.
Katul, L.; Timchenko, T.; Gronenborn, B.; Vetten, H. J.
Federal Research Centre for Agriculture and Forestry (BBA), Institute for Plant Virology, Microbiology and Biosafety, Messeweg 11-12, 38104 Braunschweig, Germany.
Conference Title: New aspects of resistance research on cultivated plants: virus diseases. Proceedings of the 7th Aschersleben Symposium, Aschersleben, Germany, 17-18 November, 1999.
Beitrage zur Zuchtungsforschung - Bundesanstalt fur Zuchtungsforschung an Kulturpflanzen vol. 6 (3): p.87-91
Publication Year: 2000
ISSN: 0948-5538 --
Language: English
Document Type: Journal article; Conference paper
Expression of dominant negative variants of the viral replication initiator **protein** (**Rep**) was applied to studying **resistance** to faba bean necrotic yellows **virus** in Vicia faba. It is suggested that the genome consists of at least 8 DNA components. The most conserved nanovirus **protein** is encoded by the master **rep** DNA which, with the 7 non-**rep** components described from a legume-infecting nanovirus isolate from Ethiopia, appear to be integral genome parts. The expression of mutated master **Rep proteins** with a dominant negative phenotype seemed promising for obtaining lines of V. faba **resistant** to faba bean necrotic yellows **virus**. 23 ref.

3/3,AB/18 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04660089 H.W. WILSON RECORD NUMBER: BGSA01160089
Hospital infection control in hematopoietic stem cell transplant recipients.
Dykewicz, Clare A
Emerging Infectious Diseases (Emerging Infect Dis) v. 7 no2 (Mar./Apr. 2001) p. 263-7
SPECIAL FEATURES: bibl f ISSN: 1080-6040
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 4619

ABSTRACT: Guidelines for Preventing Opportunistic Infections Among Hematopoietic Stem Cell Transplant Recipients contains a section on hospital infection control including evidence-based recommendations regarding ventilation, construction, equipment, **plants**, play areas and toys, health-care workers, visitors, patient skin and oral care, catheter-related infections, drug-**resistant** organisms, and specific nosocomial infections. These guidelines are intended to reduce the number and severity of hospital infections in hematopoietic stem cell transplant recipients. Reprinted by permission of the publisher.

3/3,AB/19 (Item 2 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text
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04650687 H.W. WILSON RECORD NUMBER: BGSA01150687
Good nutrition for all: challenges for the nutritional sciences in the new millennium.
Young, Vernon R
Nutrition Today (Nutr Today) v. 36 no1 (Jan./Feb. 2001) p. 6-16
SPECIAL FEATURES: bibl f graph il tab ISSN: 0029-666X
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8242

ABSTRACT: This keynote speech was presented at the beginning of the 8th Asian Congress on Nutrition in Seoul, Korea (August 27-September 2, 1999). Reprinted by permission of the publisher.

3/3,AB/20 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2001 The HW Wilson Co. All rts. reserv.

04508076 H.W. WILSON RECORD NUMBER: BGSA01008076
Surfactant **proteins** A and D and pulmonary host defense.
Crouch, Erika
Wright, Jo Rae
Annual Review of Physiology v. 63 (2001) p. 521-54
SPECIAL FEATURES: bibl il ISSN: 0066-4278
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 15535

ABSTRACT: The lung collectins, SP-A and SP-D, are important components of the innate immune response to microbial challenge and participate in other aspects of immune and inflammatory regulation within the lung. Both **proteins** bind to surface structures expressed by a wide variety of microorganisms and have the capacity to modulate multiple leukocyte functions, including the enhanced internalization and killing of certain microorganisms in vitro. In addition, transgenic mice with deficiencies in SP-A and SP-D show defective or altered responses to challenge with bacterial, fungal, and viral microorganisms and to bacterial lipoplysaccharides in vivo. Thus collectins could play particularly important roles in settings of inadequate or impaired specific immunity, and acquired alternations in the levels of active collectins within the airspaces and distal airways may increase susceptibility to infection. Reprinted by permission of the publisher.

3/3,AB/21 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2001 The HW Wilson Co. All rts. reserv.

04274010 H.W. WILSON RECORD NUMBER: BGSA00024010
Iron metabolism in pathogenic bacteria.
Ratledge, Colin
Dover, Lynn G
Annual Review of Microbiology v. 54 (2000) p. 881-941
SPECIAL FEATURES: bibl diag tab ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 29223

ABSTRACT: The ability of pathogens to obtain iron from transferrins, ferritin, hemoglobin, and other iron-containing **proteins** of their host is central to whether they live or die. To combat invading bacteria,

animals go into an iron-withholding mode and also use a **protein** (Nramp1) to generate reactive oxygen species in an attempt to kill the pathogens. Some invading bacteria respond by producing specific iron chelators--siderophores--that remove the iron from the host sources. Other bacteria rely on direct contact with host iron **proteins**, either abstracting the iron at their surface or, as with heme, taking it up into the cytoplasm. The expression of a large number of genes (>40 in some cases) is directly controlled by the prevailing intracellular concentration of Fe(II) via its complexing to a regulatory **protein** (the Fur **protein** or equivalent). In this way, the biochemistry of the bacterial cell can accommodate the challenges from the host. Agents that interfere with bacterial iron metabolism may prove extremely valuable for chemotherapy of diseases. Reprinted by permission of the publisher.

3/3,AB/22 (Item 5 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04273987 H.W. WILSON RECORD NUMBER: BGSA00023987
Microbiological safety of drinking water.
Szewzyk, U
Szewzyk, R; Manz, W
Annual Review of Microbiology v. 54 (2000) p. 81-127
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 23990

ABSTRACT: Emerging pathogens in drinking water have become increasingly important during the decade. These include newly-recognized pathogens from fecal sources such as Cryptosporidium parvum, Campylobacter spp., and rotavirus, as well as pathogens that are able to grow in water distribution systems, like Legionella spp., mycobacteria, and aeromonads. To perform a risk analysis for the pathogens in drinking water, it is necessary to understand the ecology of these organisms. The ecology of the drinking-water distribution system has to be evaluated in detail, especially the diversity and physiological properties of water bacteria. The interactions between water bacteria and (potential) pathogens in such diverse habitats as free water and biofilms are essential for the survival or growth of hygienically relevant organisms in drinking water. Results of epidemiological studies together with ecological data are the basis for effective resource protection, water treatment, and risk assessment. Reprinted by permission of the publisher.

3/3,AB/23 (Item 6 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04255640 H.W. WILSON RECORD NUMBER: BGSA00005640
Plant retrotransposons.
AUGMENTED TITLE: review
Kumar, Amar
Bennetzen, Jeffrey L
Annual Review of Genetics v. 33 (1999) p. 479-532
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 22407

ABSTRACT: Retrotransposons are mobile genetic elements that transpose through reverse transcription of an RNA intermediate. Retrotransposons are ubiquitous in **plants** and play a major role in **plant** gene and genome evolution. In many cases, retrotransposons comprise over 50% of

nuclear DNA content, a situation that can arise in just a few million years. **Plant** retrotransposons are structurally and functionally similar to the retrotransposons and retroviruses that are found in other eukaryotic organisms. However, there are important differences in the genomic organization of retrotransposons in **plants** compared to some other eukaryotes, including their often-high copy numbers, their extensively heterogeneous populations, and their chromosomal dispersion patterns. Recent studies are providing valuable insights into the mechanisms involved in regulating the expression and transposition of retrotransposons. This review describes the structure, genomic organization, expression, regulation, and evolution of retrotransposons, and discusses both their contributions to **plant** genome evolution and their use as genetic tools in **plant** biology. Reprinted by permission of the publisher.

3/3,AB/24 (Item 7 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04250995 H.W. WILSON RECORD NUMBER: BGSA00000995
Evolutionary computation: an overview.
Mitchell, Melanie
Taylor, Charles E
Annual Review of Ecology and Systematics v. 30 (1999) p. 593-616
SPECIAL FEATURES: bibl il ISSN: 0066-4162
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11547

ABSTRACT: The current state of the field of evolutionary computation is reviewed. Evolutionary computation is a section of computer science that uses ideas from biological evolution to resolve computational problems. Evolutionary computation is best suited to problems that involve nonlinear interactions among numerous elements, that have many intermediate optima, and whose solutions are very good without necessarily being the absolute optimum. Genetic algorithms are the most widely used approach in the field of evolutionary computation.

3/3,AB/25 (Item 8 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04101441 H.W. WILSON RECORD NUMBER: BGSA99101441
Environmental chemical exposures and risk of herpes zoster.
Arndt, Volker
Vine, Marilyn F; Weigle, Kristen
Environmental Health Perspectives (Environ Health Perspect) v. 107 no10 (Oct. 1999) p. 835-41
SPECIAL FEATURES: bibl il ISSN: 0091-6765
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6224

ABSTRACT: This study investigated whether residence in Aberdeen, North Carolina, the location of the Aberdeen pesticides dumps site (a national priority list Superfund site containing organochlorine pesticides, volatile organic compounds, and metals), is associated with immune suppression as indicated by a higher incidence of herpes zoster and recent occurrences of other common infectious diseases. Study participants included 1,642 residents, 18-64 years of age, who responded to a telephone survey concerning potential occupational and recreational exposures to pesticides and other chemicals, lifetime history of herpes zoster (shingles), and the recent occurrence of other common infectious diseases. Stratified and

logistic regression analyses were used to compare the cumulative incidence of herpes zoster among Aberdeen residents and residents of nearby communities. There was little evidence of an overall increased risk of herpes zoster among Aberdeen residents during the period 1951-1994 (relative risk (RR), 1.3; 95% confidence interval (CI), 0.8-2.1). However, an elevated risk of herpes zoster was noted consistently among Aberdeen residents of younger ages as compared to residents of the nearby communities. The RR was 2.0 (CI, 1.0-4.0) among those 18-40 years of age and was not affected by controlling for potential confounders. The RR of herpes zoster was also consistently elevated in all age groups for the period before 1985. No differences were noted between residents of Aberdeen and those of the nearby communities with respect to the recent occurrence of other common infectious diseases. These results support the plausibility of an association between exposure to the Aberdeen pesticides dumps site and immune suppression and the potential use of herpes zoster as a marker of immune suppression in studies of environmental chemical exposures. Key words. environmental, hazardous waste, herpes zoster, immune suppression, organochlorine, shingles. Environ Health Perspect 107:835-841 (1999). [Online 9 September 1999] Reprinted by permission of the publisher.

3/3,AB/26 (Item 9 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04101403 H.W. WILSON RECORD NUMBER: BGSA99101403
Ancient-modern concordance in Ayurvedic **plants**: some examples.
Dev, Sukh
Environmental Health Perspectives (Environ Health Perspect) v. 107 no10 (Oct. 1999) p. 783-9
SPECIAL FEATURES: bibl il ISSN: 0091-6765
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7561

ABSTRACT: Ayurveda is the ancient (before 2500 B.C.) Indian system of health care and longevity. It involves a holistic view of man, his health, and illness. Ayurvedic treatment of a disease consists of salubrious use of drugs, diets, and certain practices. Medicinal preparations are invariably complex mixtures, based mostly on **plant** products. Around 1,250 **plants** are currently used in various Ayurvedic preparations. Many Indian medicinal **plants** have come under scientific scrutiny since the middle of the nineteenth century, although in a sporadic fashion. The first significant contribution from Ayurvedic materia medica came with the isolation of the hypertensive alkaloid from the sarpagandha **plant** (Rauwolfia serpentina), valued in Ayurveda for the treatment of hypertension, insomnia, and insanity. This was the first important ancient-modern concordance in Ayurvedic **plants**. With the gradual coming of age of chemistry and biology, disciplines central to the study of biologic activities of natural products, many Ayurvedic **plants** have been reinvestigated. Our work on Commiphora wightti gum-resin, valued in Ayurveda for correcting lipid disorders, has been described in some detail; based on these investigations, a modern antihyperlipoproteinemic drug is on the market in India and some other countries. There has also been concordance for a few other Ayurvedic crude drugs such as Asparagus racemosus, Cedrus deodara, and Psoralea corylifolia. Key words: c-aminobutyric acid, antihyperlipoproteinemic drug, Asparagus racemosus, Ayurveda, bakuchiol, Cedrus deodara, Commiphora wightti, GABA, guggulsterones, himachalol, Psoralea corylifolia, reserpine, Rauwolfia serpentina. Environ Health Perspect 107:783-789 (1999). [Online 25 August 1999] Reprinted by permission of the publisher.

3/3,AB/27 (Item 10 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04050512 H.W. WILSON RECORD NUMBER: BGSA99050512
Transmissible spongiform encephalopathies in humans.
AUGMENTED TITLE: review
Belay, Ermias D
Annual Review of Microbiology v. 53 (1999) p. 283-314
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13838

ABSTRACT: Creutzfeldt-Jakob disease (CJD), the first transmissible spongiform encephalopathy (TSE) to be described in humans, occurs in a sporadic, familial, or iatrogenic form. Other TSEs in humans, shown to be associated with specific prion **protein** gene mutations, have been reported in different parts of the world. These TSEs compose a heterogeneous group of familial diseases that traditionally have been classified as familial CJD, Gerstmann-Straussler-Scheinker syndrome, or fatal familial insomnia. In 1996, a newly recognized variant form of CJD among young patients (median age, 28 years) with unusual clinical features and a unique neuropathologic profile was reported in the United Kingdom. In the absence of known CJD risk factors or prion **protein** gene abnormalities, the UK government concluded that the clustering of these cases may represent transmission to humans of the agent causing bovine spongiform encephalopathy. Additional epidemiologic and recent laboratory data strongly support the UK government's conclusion. Reprinted by permission of the publisher.

3/3,AB/28 (Item 11 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04045917 H.W. WILSON RECORD NUMBER: BGSI99045917
eIF4 initiation factors: effectors of mRNA recruitment to ribosomes and regulators of translation.
Gingras, Anne-Claude
Raught, Brian; Sonenberg, Nahum
Annual Review of Biochemistry v. 68 (1999) p. 913-63
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 21787

ABSTRACT: Eukaryotic translation initiation factor 4F (eIF4F) is a **protein** complex that mediates recruitment of ribosomes to mRNA. This event is the rate-limiting step for translation under most circumstances and a primary target for translational control. Functions of the constituent **proteins** of eIF4F include recognition of the mRNA 5' cap structure (eIF4E), delivery of an RNA helicase to the 5' region (eIF4A), bridging of the mRNA and the ribosome (eIF4G), and circularization of the mRNA via interaction with poly(A)-binding **protein** (eIF4G). eIF4 activity is regulated by transcription, phosphorylation, **inhibitory proteins**, and proteolytic cleavage. Extracellular stimuli evoke changes in phosphorylation that influence eIF4F activity, especially through the phosphoinositide 3-kinase (PI3K) and Ras signaling pathways. Viral infection and cellular stresses also affect eIF4F function. The recent determination of the structure of eIF4E at atomic resolution has provided insight about how translation is initiated and regulated. Evidence suggests that eIF4F is also implicated in malignancy and apoptosis. Reprinted by permission of the publisher.

3/3,AB/29 (Item 12 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text

04036660 H.W. WILSON RECORD NUMBER: BGSI99036660
Health care worker disability due to latex allergy and asthma: a cost analysis.
Phillips, V. L
Goodrich, Martha A; Sullivan, Timothy J
American Journal of Public Health (Am J Public Health) v. 89 no7 (July 1999) p. 1024-8
SPECIAL FEATURES: bibl il ISSN: 0090-0036
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 3687

ABSTRACT: Objectives. The reported prevalence of occupational allergy to natural rubber latex is 8% to 17%, and that of latex-induced occupational asthma is 2.5% to 6%. Conversion of medical facilities to "latex-safe" can reduce employee sensitization, impairment, and disability. The purpose of this study was to determine the cost of a latex-safe approach, compared with that of continued latex glove use, and to identify the level of worker disability required to make the latex-safe approach financially preferable to a health care institution. Methods. The costs of 2 strategies--latex-safe vs the status quo--were calculated from the perspective of 3 health care institutions. A break-even point was calculated for each facility. Results. In all facilities, the cost of using nonlatex gloves exceeded the cost of using latex gloves. In all 3 facilities, however, 1% or fewer of those at risk would have to become fully disabled or fewer than 2% would have to become partially disabled for the continued use of latex gloves to exceed the cost of the latex-safe approach. Conclusion. Health care facilities, regardless of size, are likely to benefit financially from becoming latex-safe even if latex-related disability levels are extremely low. (Am J Public Health. 1999;89:1024-1028) Reprinted by permission of the publisher.

3/3,AB/30 (Item 13 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04007261 H.W. WILSON RECORD NUMBER: BGSI99007261
Bacterial symbiosis in arthropods and the control of disease transmission.
Beard, Charles B
Durvasula, Ravi V; Richards, Frank F
Emerging Infectious Diseases (Emerging Infect Dis) v. 4 no4 (Oct./Dec. '98) p. 581-91
SPECIAL FEATURES: bibl il ISSN: 1080-6040
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6897

ABSTRACT: Bacterial symbionts may be used as vehicles for expressing foreign genes in arthropods. Expression of selected genes can render an arthropod incapable of transmitting a second microorganism that is pathogenic for humans and is an alternative approach to the control of arthropod-borne diseases. We discuss the rationale for this alternative approach, its potential applications and limitations, and the regulatory concerns that may arise from its use in interrupting disease transmission in humans and animals. Reprinted by permission of the publisher.

3/3,AB/31 (Item 14 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04004113 H.W. WILSON RECORD NUMBER: BGSI99004113
Nonsegmented negative-st[redacted]d RNA **viruses**: genetics and m[redacted]ulation of viral genomes.
Conzelmann, Karl-Klaus
Annual Review of Genetics (Annu Rev Genet) v. 32 ('98) p. 123-62
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 19760

ABSTRACT: The genetics and manipulation of nonsegmented negative-strand RNA **viruses** (NSVs) are discussed. Protocols that have been developed to recover NSVs entirely from cDNA have opened up this group of **viruses** to detailed molecular genetic and **virus** biology analyses. The gene-expression strategy of nonsegmented NSVs involves the replication of ribonucleoprotein complexes and sequential synthesis of free mRNA. This strategy permits the use of NSVs to express heterologous sequences and has definite advantages in terms of easy manipulation of constructs, high capacity for foreign sequences, genetically stable expression, and the possibility of controlling the levels of expression. Furthermore, chimeric **virus** vectors carrying novel envelope **protein** genes and targeted to defined host cells offer interesting prospects for biomedical applications and transient gene therapy.

3/3,AB/32 (Item 15 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03795782 H.W. WILSON RECORD NUMBER: BGSI98045782
Wild primate populations in emerging infectious disease research: the missing link?.
Wolfe, Nathan D
Escalante, Ananias A; Karesh, William B
Emerging Infectious Diseases (Emerging Infect Dis) v. 4 no2 (Apr./June '98) p. 149-58
SPECIAL FEATURES: bibl il ISSN: 1080-6040
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6381

ABSTRACT: Wild primate populations, an unexplored source of information regarding emerging infectious disease, may hold valuable clues to the origins and evolution of some important pathogens. Primates can act as reservoirs for human pathogens. As members of biologically diverse habitats, they serve as sentinels for surveillance of emerging pathogens and provide models for basic research on natural transmission dynamics. Since emerging infectious diseases also pose serious threats to endangered and threatened primate species, studies of these diseases in primate populations can benefit conservation efforts and may provide the missing link between laboratory studies and the well-recognized needs of early disease detection, identification, and surveillance. Reprinted by permission of the publisher.

3/3,AB/33 (Item 16 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03751705 H.W. WILSON RECORD NUMBER: BGSI98001705
Genetic analysis of chlorophyll biosynthesis.
AUGMENTED TITLE: bacterial, algal and **plant**
Suzuki, Jon Y
Bollivar, David W; Bauer, Carl E
Annual Review of Genetics (Annu Rev Genet) v. 31 ('97) p. 61-89

SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11704

ABSTRACT: The Mg-tetrapyrroles bacteriochlorophyll a and chlorophyll a are discussed. The biosynthetic pathways of these 2 Mg-tetrapyrroles use common intermediates from Mg-protoporphyrin IX through chlorophyllide a. The majority of the different bacteriochlorophylls and chlorophylls that are synthesized by bacterial, algal, and **plant** photosynthetic organisms seem to use similar early metabolic intermediates, indicating that the different end products are variants of an evolutionarily conserved biosynthetic pathway. There is extensive sequence homology among the enzymes that catalyze similar steps in chlorophyll a and bacteriochlorophyll a biosynthetic pathways, which indicates that these pathways share a common ancestry.

3/3,AB/34 (Item 17 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03751693 H.W. WILSON RECORD NUMBER: BGSI98001693
Evolutionary genetics of life cycles.
Kondrashov, Alexey S
Annual Review of Ecology and Systematics (Annu Rev Ecol Syst) v. 28 ('97) p. 391-435
SPECIAL FEATURES: bibl ISSN: 0066-4162
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 21636

ABSTRACT: Progress on understanding the life cycles of cellular species from the viewpoint of transmission genetics and evolution is reviewed. Although there is a good deal of information available on the life cycles of **plants**, animals, and, to a lesser extent, other multicellular eukaryotes, the life cycles of prokaryotes and unicellular eukaryotes have been studied insufficiently. More data are required on the molecular architecture of meiosis in various taxa and on the genetic structures of protozoan populations and on their phylogeny. Much theoretical work remains to be carried out before it is clear whether any transmission genetic factors can explain obligate amphimixis. Further study also needs to be conducted on the physiological effects of various life cycle features and the parameters relevant to population genetic theory.

3/3,AB/35 (Item 18 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03293634 H.W. WILSON RECORD NUMBER: BGSI96043634
My role in the discovery and classification of the enteroviruses.
Melnick, Joseph L
Annual Review of Microbiology (Annu Rev Microbiol) v. 50 ('96) p. 1-24
SPECIAL FEATURES: bibl il por ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11867

ABSTRACT: The enteroviruses constitute one of the genera of the picomavirus family. The genus includes the polioviruses, the coxsackieviruses, and the echoviruses of humans, plus a number of enteroviruses of lower animals (e.g. monkeys, cattle, pigs, mice). Over 100 serotypes are recognized, of which the first to be discovered were the polioviruses. It was my good fortune to have been a scientist during the

golden age of virology, when new techniques were being introduced into the field. These often led to the discovery of new **viruses**. This article details the isolation of the enteroviruses, their recognition as a separate genus of Picornaviridae, and my role in the process. Poliovirus, the most hazardous of the group, is almost gone from the world, but the other enteroviruses will be with us for some time. Several members of the Committee dealing with these agents--Enders, Sabin, Dalldorf, Syverton--have passed on, but the work of this Committee to which I was privileged to contribute will live long. Reprinted by permission of the publisher.

3/3,AB/36 (Item 19 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03254134 H.W. WILSON RECORD NUMBER: BGSI96004134
False positive tuberculosis skin test results.
Grabau, John C
DiFerdinando, George T.,Jr; Novick, Lloyd F
Public Health Reports (Public Health Rep) v. 110 (Nov./Dec. '95) p. 703-6
DOCUMENT TYPE: Feature Article
SPECIAL FEATURES: bibl il ISSN: 0033-3549
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 2997

ABSTRACT: Several clusters of false positive tuberculin skin testing (TST) results have recently been associated with one brand of purified **protein** derivative (PPD). The false positive reactions occurred in New York State during a brief period in 1992. The clustering of unanticipated positive TSTs in several different locations, occurring over a short period of time with what appeared to be a small number of production lots, indicated that problems with the testing solution were likely. Investigations suggested that the high rates of false positivity were associated with the use of product S (Sclavo, Sclavo), and the manufacturer subsequently removed the product from the market.

3/3,AB/37 (Item 20 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

03253299 H.W. WILSON RECORD NUMBER: BGSI96003299
Light-harvesting complexes in oxygenic photosynthesis: diversity, control, and evolution.
Grossman, Arthur R
Bhaya, Devaki; Apt, Kirk E
Annual Review of Genetics (Annu Rev Genet) v. 29 ('95) p. 231-88
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 27752

ABSTRACT: The light-harvesting complexes (LHCs) in oxygen-evolving, photosynthetic organisms are reviewed. These organisms include **plants**, cyanobacteria, diatoms, chrysophytes, dinoflagellates, and red, green, and brown algae. The LHCs represent a diverse range of pigment-**protein** complexes that facilitate the conversion of radiant energy to chemical bond energy. The synthesis of LHCs is regulated by environmental parameters such as light and nutrients. There are several evolutionary relationships among the LHC structural polypeptides.

3/3,AB/38 (Item 21 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text
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03253291 H.W. WILSON RECORD NUMBER: BGSI96003291
The **plant** response in pathogenesis, symbiosis, and wounding: variations on a common theme?.
Baron, C
Zambryski, P. C
Annual Review of Genetics (Annu Rev Genet) v. 29 ('95) p. 107-29
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10748

ABSTRACT: Current knowledge of the **plant** reaction to apparently different biotic and abiotic stimuli is reviewed. **Plants** act in superficially different ways upon interaction with pathogenic Pseudomonads or symbiotic Rhizobia or after wounding by abrasion or insects. The injury results in either a close association with or a defense against the intruder. However, closer examination reveals that similar genes and metabolic pathways are induced by injury, suggesting that signal perception and transduction proceed via similar pathways. These similarities lead to overlaps in the response reaction. Therefore, within the course of evolution, similar response mechanisms were adapted to specific needs.

3/3,AB/39 (Item 22 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03051092 H.W. WILSON RECORD NUMBER: BGSI95051092
Environmental virology: from detection of **virus** in sewage and water by isolation to identification by molecular biology--a trip of over 50 years.
Metcalf, T. G
Melnick, J. L; Estes, M. K
Annual Review of Microbiology (Annu Rev Microbiol) v. 49 ('95) p. 461-87
DOCUMENT TYPE: Feature Article
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12950

ABSTRACT: Environmental virology began with efforts to detect poliovirus in sewage and water more than 50 years ago. Since that time, cell-culture methods useful for detection of enteroviruses have been replaced by molecular biology techniques for detection of pathogens (hepatitis A and E **viruses**, caliciviruses, rotaviruses, and astroviruses) that do not grow in cell culture or grow with great difficulty. Amplification of viral nucleic acid using the polymerase chain reaction (PCR) is the current preferred method. PCR or RT-PCR (to detect RNA viral genomes) is rapid, sensitive, specific, and quantitative. Method shortcomings include potential **inhibition** by substances in some environmental samples and an inability of test results to distinguish between infectious and noninfectious **virus**. Current questions involving use of PCR/RT-PCR tests for public health purposes include: What is the public health significance of a positive test, and should direct tests for **viruses** replace current public health-monitoring programs? Reprinted by permission of the publisher.

3/3,AB/40 (Item 23 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03051090 H.W. WILSON RECORD NUMBER: BGSI95051090
New mechanisms of drug **resistance** in parasitic protozoa.
Borst, P
Ouellette, M
Annual Review of Microbiology (Annu Rev Microbiol) v. 49 ('95) p. 427-60
DOCUMENT TYPE: Feature Article
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 15781

ABSTRACT: The main line of defense now available against parasitic protozoa--which are responsible for major diseases of humans and domestic animals--is chemotherapy. This defense is being eroded by drug **resistance** and, with few new drugs in the pipeline, prevention and circumvention of **resistance** are medical and veterinary priorities. Although studies of **resistance** mechanisms in parasites have lagged behind similar studies in bacteria and cancer cells, the tools to tackle this problem are rapidly improving. Transformation with exogenous DNA is now possible with all major parasitic protozoa of humans. Hence, putative **resistance** genes can be tested in sensitive protozoa, allowing an unambiguous reconstruction of **resistance** mechanisms. Gene cloning, the polymerase chain reaction, and monoclonal antibodies against **resistance**-related **proteins** have made it possible to analyze potential **resistance** mechanisms in the few parasites that can be obtained from infected people. Hence, the prospect of applying new knowledge about **resistance** mechanisms to parasites in patients is good, even though today virtually all knowledge pertains to parasites selected for **resistance** in the laboratory. **Resistance** mechanisms highlighted in this review include: 1. Decrease of drug uptake because of the loss of a transporter required for uptake. This decrease contributes to **resistance** to arsenicals and diamidines in African trypanosomes. 2. The export of drugs from the parasite by P-glycoproteins and other traffic ATPases. This export could potentially be an important mechanism of **resistance**, as these **proteins** are richly represented in the few protozoa analyzed. There are indications that such transmembrane transporters can be involved in **resistance** to emetine in Entamoeba spp., to mefloquine in Plasmodium spp., and to antimonials in Leishmania spp. 3. The possible involvement of the P-glycoprotein encoded by the Plasmodium falciparum pfmdr1 gene in chloroquine **resistance**. We present the available data that lead to the conclusion that overproduction of the wild-type version of this **protein** results in chloroquine hypersensitivity rather than **resistance**. 4. The involvement of the PgpA P-glycoprotein of Leishmania spp. in low-level **resistance** to arsenite and antimonials. We raise the possibility that this **protein** transports glutathione conjugates of arsenite and antimonials rather than the compounds themselves. 5. Loss of drug activation as the main mechanism of metronidazole **resistance** in Trichomonas and Giardia spp. Recent evidence indicates that a decrease of the proximal cellular electron donor for metronidazole activation, ferredoxin, is the main cause of **resistance** in Trichomonas. 6. **Resistance** arising through alteration of drug targets. The amino acid substitutions in the dihydrofolate reductase-thymidylate synthase of Plasmodium spp. are good examples of this mechanism. We show here that the field of drug **resistance** in parasitic protozoa is currently very active and holds considerable future opportunity. With the tools now available, progress should be rapid in the coming years. Reprinted by